SEQUENCE LISTING

<110> MIYATA, Toshio
      KUROKAWA, Kiyoshi

<120> Meg-3 protein

<130> 2605/101

<140> 10/018,311
<141> 2000-4-28

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3768
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 3395, 3437, and 3440
<223> N=G,A,C or T

<400> 1
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caggaactgg gccagctccg gtcccttcct tttggggctc tcactctgga gg atg ggg 58
                                                          Met Gly
                                                           1


tgg atg gga gaa aaa acc ggg aag atc ctg acg gag ttc ctc cag ttc     106
Trp Met Gly Glu Lys Thr Gly Lys Ile Leu Thr Glu Phe Leu Gln Phe
          5                  10                  15


tat gaa gac cag tat ggc gtg gct ctc ttc aac agc atg cgc cat gag     154
Tyr Glu Asp Gln Tyr Gly Val Ala Leu Phe Asn Ser Met Arg His Glu
     20                  25                  30


att gag ggc acg ggg ctg ccg cag gcc cag ctg ctc tgg cgc aag gtg     202
Ile Glu Gly Thr Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg Lys Val
 35                  40                  45                  50


cca ctg gac gag cgc atc gtc ttc tcg ggg aac ctc ttc cag cac cag     250
Pro Leu Asp Glu Arg Ile Val Phe Ser Gly Asn Leu Phe Gln His Gln
                 55                  60                  65


gag gac agc aag aag tgg aga aac cgc ttc agc ctc gtg ccc cac aac     298
Glu Asp Ser Lys Lys Trp Arg Asn Arg Phe Ser Leu Val Pro His Asn
                 70                  75                  80


tac ggg ctg gtg ctc tac gaa aac aaa gcg gcc tat gag cgg cag gtc     346
Tyr Gly Leu Val Leu Tyr Glu Asn Lys Ala Ala Tyr Glu Arg Gln Val
             85                  90                  95
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1

cca cca cga gcc gtc atc aac agt gca ggc tac aaa atc ctc acg tcc   394
Pro Pro Arg Ala Val Ile Asn Ser Ala Gly Tyr Lys Ile Leu Thr Ser
100   105   110

gtg gac caa tac ctg gag ctc att ggc aac tcc tta cca ggg acc acg   442
Val Asp Gln Tyr Leu Glu Leu Ile Gly Asn Ser Leu Pro Gly Thr Thr
115   120   125   130

gca aag tcg ggc agt gcc ccc atc ctc aag tgc ccc aca cag ttc ccg   490
Ala Lys Ser Gly Ser Ala Pro Ile Leu Lys Cys Pro Thr Gln Phe Pro
             135   140   145

ctc atc ctc tgg cat cct tat gcg cgt cac tac tac ttc tgc atg atg   538
Leu Ile Leu Trp His Pro Tyr Ala Arg His Tyr Tyr Phe Cys Met Met
             150   155   160

aca gaa gcc gag cag gac aag tgg cag gct gtg ctg cag gac tgc atc   586
Thr Glu Ala Glu Gln Asp Lys Trp Gln Ala Val Leu Gln Asp Cys Ile
             165   170   175

cgg cac tgc aac aat gga atc cct gag gac tcc aag gta gag ggc cct   634
Arg His Cys Asn Asn Gly Ile Pro Glu Asp Ser Lys Val Glu Gly Pro
             180   185   190

gcg ttc aca gat gcc atc cgc atg tac cga cag tcc aag gag ctg tac   682
Ala Phe Thr Asp Ala Ile Arg Met Tyr Arg Gln Ser Lys Glu Leu Tyr
195   200   205   210

ggc acc tgg gag atg ctg tgt ggg aac gag gtg cag atc ctg agc aac   730
Gly Thr Trp Glu Met Leu Cys Gly Asn Glu Val Gln Ile Leu Ser Asn
                 215   220   225

ctg gtg atg gag gag ctg ggc cct gag ctg aag gca gag ctc ggc ccg   778
Leu Val Met Glu Glu Leu Gly Pro Glu Leu Lys Ala Glu Leu Gly Pro
             230   235   240

cgg ctg aag ggg aaa ccg cag gag cgg cag cgg cag tgg atc cag atc   826
Arg Leu Lys Gly Lys Pro Gln Glu Arg Gln Arg Gln Trp Ile Gln Ile
             245   250   255

tcg gac gcc gtg tac cac atg gtg tac gag cag gcc aag gcg cgc ttc   874
Ser Asp Ala Val Tyr His Met Val Tyr Glu Gln Ala Lys Ala Arg Phe
             260   265   270

gag gag gtg ctg tcc aag gtg cag cag gtg cag ccg gcc atg cag gcc   922
Glu Glu Val Leu Ser Lys Val Gln Gln Val Gln Pro Ala Met Gln Ala
275   280   285   290

gtc atc cga act gac atg gac caa att atc acc tcc aag gag ctc ctt   970
Val Ile Arg Thr Asp Met Asp Gln Ile Ile Thr Ser Lys Glu Leu Leu
                 295   300   305

gcc agc aag atc cga gcc ttc atc ctc ccc aag gca gag gtg tgc gtg   1018
Ala Ser Lys Ile Arg Ala Phe Ile Leu Pro Lys Ala Glu Val Cys Val
             310   315   320

```
cgg aac cat gtc cag ccc tac atc cca tcc atc ctg gag gcc ctg atg       1066
Arg Asn His Val Gln Pro Tyr Ile Pro Ser Ile Leu Glu Ala Leu Met
        325             330             335

gtc ccc acc agc cag ggc ttc act gag gtg cga gat gtc ttc ttc aag       1114
Val Pro Thr Ser Gln Gly Phe Thr Glu Val Arg Asp Val Phe Phe Lys
        340             345             350

gag gtc acg gac atg aac ctg aac gtc atc aac gag ggc ggc att gac       1162
Glu Val Thr Asp Met Asn Leu Asn Val Ile Asn Glu Gly Gly Ile Asp
355             360             365             370

aag ctg ggc gag tac atg gag aag ctg tcc cgg ctg gcg tac cac ccc       1210
Lys Leu Gly Glu Tyr Met Glu Lys Leu Ser Arg Leu Ala Tyr His Pro
                375             380             385

ctg aag atg cag agc tgc tat gag aag atg gag tcg ctg cga ctg gac       1258
Leu Lys Met Gln Ser Cys Tyr Glu Lys Met Glu Ser Leu Arg Leu Asp
            390             395             400

ggg ctg cag cag cga ttt gat gtg tcc agc acg tcc gtg ttc aag cag       1306
Gly Leu Gln Gln Arg Phe Asp Val Ser Ser Thr Ser Val Phe Lys Gln
            405             410             415

cga gcc cag atc cac atg cgg gag caa atg gac aat gcc gtg tat acg       1354
Arg Ala Gln Ile His Met Arg Glu Gln Met Asp Asn Ala Val Tyr Thr
        420             425             430

ttc gag acc ctc ctg cac cag gag ctg ggg aag ggg ccc acc aag gag       1402
Phe Glu Thr Leu Leu His Gln Glu Leu Gly Lys Gly Pro Thr Lys Glu
435             440             445             450

gag ctg tgc aag tcc atc cag cgg gtc ctg gag cgg gtg ctg aaa aaa       1450
Glu Leu Cys Lys Ser Ile Gln Arg Val Leu Glu Arg Val Leu Lys Lys
                455             460             465

tac gac tac gac agc agc tct gtg cgg aag agg ttc ttc cgg gag gcg       1498
Tyr Asp Tyr Asp Ser Ser Ser Val Arg Lys Arg Phe Phe Arg Glu Ala
                470             475             480

ctg ctg cag atc agc atc ccg ttc ctg ctc aag aag ctg gcc cct acc       1546
Leu Leu Gln Ile Ser Ile Pro Phe Leu Leu Lys Lys Leu Ala Pro Thr
            485             490             495

tgc aag tcg gag ctg ccc cgg ttc cag gag ctg atc ttc gag gac ttt       1594
Cys Lys Ser Glu Leu Pro Arg Phe Gln Glu Leu Ile Phe Glu Asp Phe
        500             505             510

gcc agg ttc atc ctg gtg gaa aac acg tac gag gag gtg gtg ctg cag       1642
Ala Arg Phe Ile Leu Val Glu Asn Thr Tyr Glu Glu Val Val Leu Gln
515             520             525             530

acc gtc atg aag gac atc ctg cag gct gtg aag gag gcg gcg gtg cag       1690
Thr Val Met Lys Asp Ile Leu Gln Ala Val Lys Glu Ala Ala Val Gln
            535             540             545
```

3

```
agg aag cac aac ctc tac cgg gac agc atg gtc atg cac aac agc gac    1738
Arg Lys His Asn Leu Tyr Arg Asp Ser Met Val Met His Asn Ser Asp
            550                 555                 560

ccc aac ctg cac ctg ctg gcc gag ggc gcc ccc atc gac tgg ggc gag    1786
Pro Asn Leu His Leu Leu Ala Glu Gly Ala Pro Ile Asp Trp Gly Glu
            565                 570                 575

gag tac agc aac agc ggc ggg ggc ggc agc ccc agc ccc agc acc ccg    1834
Glu Tyr Ser Asn Ser Gly Gly Gly Gly Ser Pro Ser Pro Ser Thr Pro
        580                 585                 590

gag tca gcc acc ctc tcg gaa aag cga cgg cgc gcc aag cag gtg gtc    1882
Glu Ser Ala Thr Leu Ser Glu Lys Arg Arg Arg Ala Lys Gln Val Val
595                 600                 605                 610

tct gtg gtc cag gat gag gag gtg ggg ctg ccc ttt gag gct agc cct    1930
Ser Val Val Gln Asp Glu Glu Val Gly Leu Pro Phe Glu Ala Ser Pro
                615                 620                 625

gag tca cca cca cct gcg tcc ccg gac ggt gtc act gag atc cga ggc    1978
Glu Ser Pro Pro Pro Ala Ser Pro Asp Gly Val Thr Glu Ile Arg Gly
                630                 635                 640

ctg ctg gcc caa ggt ctg cgg cct gag agc ccc cca cca gcc ggc ccc    2026
Leu Leu Ala Gln Gly Leu Arg Pro Glu Ser Pro Pro Pro Ala Gly Pro
            645                 650                 655

ctg ctc aac ggg gcc ccc gct ggg gag agt ccc cag cct aag gcc gcc    2074
Leu Leu Asn Gly Ala Pro Ala Gly Glu Ser Pro Gln Pro Lys Ala Ala
        660                 665                 670

ccc gag gcc tcc tcg ccg cct gcc tca ccc ctc cag cat ctc ctg cct    2122
Pro Glu Ala Ser Ser Pro Pro Ala Ser Pro Leu Gln His Leu Leu Pro
675                 680                 685                 690

gga aag gct gtg gac ctt ggg ccc ccc aag ccc agc gac cag gag act    2170
Gly Lys Ala Val Asp Leu Gly Pro Pro Lys Pro Ser Asp Gln Glu Thr
                695                 700                 705

gga gag cag gtg tcc agc ccc agc agc cac ccc gcc ctc cac acc acc    2218
Gly Glu Gln Val Ser Ser Pro Ser Ser His Pro Ala Leu His Thr Thr
            710                 715                 720

acc gag gac agt gca ggg gtg cag act gag ttc taggccagtg ggtccctgac 2271
Thr Glu Asp Ser Ala Gly Val Gln Thr Glu Phe
            725                 730

tgctgcacat ggcacaggcc gttcccttcc ggacccaggc aggctcagct ctggggaggg 2331

caccctggtc tgtgccttgt gggtggaggc ggggcagggc tgtgtggcac cgccaggag 2391

cgggcccacc tgagtcactt tattgggttc agtcaacact ttcttgctcc ctgttttctc 2451

ttctgtggga tgatctcaga tgcaggggct ggttttgggg ttttcctgct tgtgccaagg 2511

gctggacact gctgggggc tggaaagccc ctccttcct gtccttctgt ggcctccatc 2571
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4

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ccctcatggg tgctgccatc cttcctggag agaggagggt gaaagctggt gtgagcccag 2631

tgggttcccg cccactcacc caggagctgg ctgggccagg accgggagag ggagcactgc 2691

tgccctcctg gccctgctcc ttccgcagtt aggggtggac cgagcctcgc tttccccact 2751

gttctggagg gaagggggaag gaggggggtct tcaggctgga gccaggctgg gggtgctggg 2811

tggagagatg agatttaggg ggtgcctcat ggggtgggca ggcctggggt gaaatgagaa 2871

aggcccagaa cgtgcaggtc tgcggagggg aagtgtcctg agtgaaggag gggaccccat 2931

cctggggatg ctgggagtga gtgagtgaga tggctgagtg agggttatgg ggagcctgag 2991

gttttatggg cctgtgtatc cccttctccc ggccccagcc tgcctccctc ctgcccgcct 3051

ggcccacagg tctccctctg gtccctgtcc ctctggtggt tggggatgga gcggcagcaa 3111

ggggtgtaat ggggctgggt tctgtcttct acaggccacc ccgaggtcct cagtggttgc 3171

ctggggagcc ggacggggct cctgagdggt acaggttggg tgggccctcc ctgagggtct 3231

ggggtcaggc tttggcctct gctgcctctc agtcaccaag tcacctccct ctgaaaatcc 3291

agtcccttct ttggatgtcc ttgtgagtca ctctgggcct ggctgtcgtc cctcctcagc 3351

ttcttgttcc tgggacaagg gtcaagccag gatgggccca ggcntgggat cccccacccc 3411

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tttgggtccc cgaggtgggg tcccctccca gccctgcatc ctccgtgccc tagacctgct 3531

ccccagagga ggggccttga cccacaggaa gtgtggtggc gcctggcaat cagggacccc 3591

cagctgccgc agccctggtt tttggcgcat cttttccctc ttgtcccgaa gatttgcgcc 3651

tttagtgcct tttgaggggt tcccatcatc cctccctgat attgtattga aaatattatg 3711

cacactgttc atgcttttac taatcaataa acgctttatt taaaaaaaaa aaaaaaa      3768
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<210> 2
<211> 733
<212> PRT
<213> Homo sapiens

<400> 2

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Met Gly Trp Met Gly Glu Lys Thr Gly Lys Ile Leu Thr Glu Phe Leu
  1               5                  10                  15

Gln Phe Tyr Glu Asp Gln Tyr Gly Val Ala Leu Phe Asn Ser Met Arg
             20                  25                  30

His Glu Ile Glu Gly Thr Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg
         35                  40                  45
```

5

```
Lys Val Pro Leu Asp Glu Arg Ile Val Phe Ser Gly Asn Leu Phe Gln
    50                  55              60

His Gln Glu Asp Ser Lys Lys Trp Arg Asn Arg Phe Ser Leu Val Pro
 65              70              75              80

His Asn Tyr Gly Leu Val Leu Tyr Glu Asn Lys Ala Ala Tyr Glu Arg
            85              90              95

Gln Val Pro Pro Arg Ala Val Ile Asn Ser Ala Gly Tyr Lys Ile Leu
            100             105             110

Thr Ser Val Asp Gln Tyr Leu Glu Leu Ile Gly Asn Ser Leu Pro Gly
        115             120             125

Thr Thr Ala Lys Ser Gly Ser Ala Pro Ile Leu Lys Cys Pro Thr Gln
        130             135             140

Phe Pro Leu Ile Leu Trp His Pro Tyr Ala Arg His Tyr Tyr Phe Cys
145             150             155             160

Met Met Thr Glu Ala Glu Gln Asp Lys Trp Gln Ala Val Leu Gln Asp
            165             170             175

Cys Ile Arg His Cys Asn Asn Gly Ile Pro Glu Asp Ser Lys Val Glu
            180             185             190

Gly Pro Ala Phe Thr Asp Ala Ile Arg Met Tyr Arg Gln Ser Lys Glu
        195             200             205

Leu Tyr Gly Thr Trp Glu Met Leu Cys Gly Asn Glu Val Gln Ile Leu
    210             215             220

Ser Asn Leu Val Met Glu Glu Leu Gly Pro Glu Leu Lys Ala Glu Leu
225             230             235             240

Gly Pro Arg Leu Lys Gly Lys Pro Gln Glu Arg Gln Arg Gln Trp Ile
            245             250             255

Gln Ile Ser Asp Ala Val Tyr His Met Val Tyr Glu Gln Ala Lys Ala
            260             265             270

Arg Phe Glu Glu Val Leu Ser Lys Val Gln Gln Val Gln Pro Ala Met
        275             280             285

Gln Ala Val Ile Arg Thr Asp Met Asp Gln Ile Ile Thr Ser Lys Glu
    290             295             300

Leu Leu Ala Ser Lys Ile Arg Ala Phe Ile Leu Pro Lys Ala Glu Val
305             310             315             320

Cys Val Arg Asn His Val Gln Pro Tyr Ile Pro Ser Ile Leu Glu Ala
            325             330             335

Leu Met Val Pro Thr Ser Gln Gly Phe Thr Glu Val Arg Asp Val Phe
            340             345             350
```

6

```
Phe Lys Glu Val Thr Asp Met Asn Leu Asn Val Ile Asn Glu Gly Gly
        355             360             365
Ile Asp Lys Leu Gly Glu Tyr Met Glu Lys Leu Ser Arg Leu Ala Tyr
        370             375             380
His Pro Leu Lys Met Gln Ser Cys Tyr Glu Lys Met Glu Ser Leu Arg
385             390             395             400
Leu Asp Gly Leu Gln Gln Arg Phe Asp Val Ser Ser Thr Ser Val Phe
                405             410             415
Lys Gln Arg Ala Gln Ile His Met Arg Glu Gln Met Asp Asn Ala Val
                420             425             430
Tyr Thr Phe Glu Thr Leu Leu His Gln Glu Leu Gly Lys Gly Pro Thr
            435             440             445
Lys Glu Glu Leu Cys Lys Ser Ile Gln Arg Val Leu Glu Arg Val Leu
    450             455             460
Lys Lys Tyr Asp Tyr Asp Ser Ser Ser Val Arg Lys Arg Phe Phe Arg
465             470             475             480
Glu Ala Leu Leu Gln Ile Ser Ile Pro Phe Leu Leu Lys Lys Leu Ala
                485             490             495
Pro Thr Cys Lys Ser Glu Leu Pro Arg Phe Gln Glu Leu Ile Phe Glu
            500             505             510
Asp Phe Ala Arg Phe Ile Leu Val Glu Asn Thr Tyr Glu Glu Val Val
            515             520             525
Leu Gln Thr Val Met Lys Asp Ile Leu Gln Ala Val Lys Glu Ala Ala
    530             535             540
Val Gln Arg Lys His Asn Leu Tyr Arg Asp Ser Met Val Met His Asn
545             550             555             560
Ser Asp Pro Asn Leu His Leu Leu Ala Glu Gly Ala Pro Ile Asp Trp
            565             570             575
Gly Glu Glu Tyr Ser Asn Ser Gly Gly Gly Gly Ser Pro Ser Pro Ser
            580             585             590
Thr Pro Glu Ser Ala Thr Leu Ser Glu Lys Arg Arg Arg Ala Lys Gln
            595             600             605
Val Val Ser Val Val Gln Asp Glu Glu Val Gly Leu Pro Phe Glu Ala
    610             615             620
Ser Pro Glu Ser Pro Pro Pro Ala Ser Pro Asp Gly Val Thr Glu Ile
625             630             635             640
Arg Gly Leu Leu Ala Gln Gly Leu Arg Pro Glu Ser Pro Pro Pro Ala
            645             650             655
```

7

```
Gly Pro Leu Leu Asn Gly Ala Pro Ala Gly Glu Ser Pro Gln Pro Lys
            660             665             670

Ala Ala Pro Glu Ala Ser Ser Pro Pro Ala Ser Pro Leu Gln His Leu
            675             680             685

Leu Pro Gly Lys Ala Val Asp Leu Gly Pro Pro Lys Pro Ser Asp Gln
      690             695             700

Glu Thr Gly Glu Gln Val Ser Ser Pro Ser Ser His Pro Ala Leu His
705             710             715             720

Thr Thr Thr Glu Asp Ser Ala Gly Val Gln Thr Glu Phe
            725             730


<210> 3
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
      Synthesized Primer Sequence

<400> 3
tgtaaaacga cggccagt                                              18


<210> 4
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
      Synthesized Primer Sequence

<400> 4
accatgatta cgccaagctt g                                          21


<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
      Synthesized Probe Sequence

<400> 5
tacctggagc tcattggcaa ctccttacca                                 30
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8

<210> 6
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
      Synthesized Primer Sequence

<400> 6
cggaattcat ggggtggatg gg   22

<210> 7
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
      Synthesized Primer Sequence

<400> 7
gcgaattcta gaactcagtc tgcacccctg c   31

<210> 8
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Artificially
      Synthesized Primer Sequence

<400> 8
gcgaattcga actcagtctg cacccctgc   29